

ABSTRACT

The presently claimed invention provides for novel methods and kits for reducing the complexity of a nucleic acid sample by providing non-gel based methods for amplification of a subset of the sequences in a sample. In a preferred embodiment, amplification of a subset can be accomplished by digesting a sample with two or more restriction enzymes and ligating adaptors to the fragments so that only a subset of the fragments can be amplified. The invention further provides for analysis of the above amplified sample by hybridization to an array, which may be specifically designed to interrogate the desired fragments for particular characteristics, such as, for example, the presence or absence of a polymorphism.

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